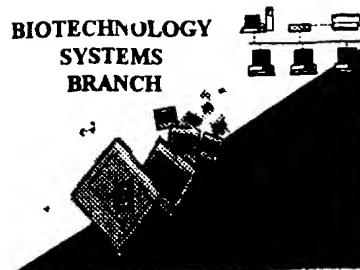


Strzelecka

#11



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/530,746
Source: 1656
Date Processed by STIC: 4/30/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY.

FOR CEF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: C9/53C, 746

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) **(2) INFORMATION FOR SEQ ID NO:X:**
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) **<210> sequence id number**
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of "Artificial" Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
(NEW RULES) Valid response is Artificial Sequence.
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
 Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing)
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1656

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/530,746

DATE: 04/30/2001
TIME: 17:59:38

Input Set : A:\4817 00.txt
Output Set: N:\CRF3\04302001\I530746.raw

pg 1-4

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Kessler, Christoph
4 Haberhausen Gerd
5 Bartl, Knut
6 Orum, Henrik
8 <120> TITLE OF INVENTION: SPECIFIC AND SENSITIVE NUCLEIC ACID DETECTION METHOD
11 <130> FILE REFERENCE: 4817/00
13 <140> CURRENT APPLICATION NUMBER: US/09/530,746
14 <141> CURRENT FILING DATE: 2000-11-16
16 <160> NUMBER OF SEQ ID NOS: 94
18 <170> SOFTWARE: PatentIn Version 3.0

ERRORED SEQUENCES

248 <210> SEQ ID NO: 21
249 <211> LENGTH: 21
250 <212> TYPE: DNA
C--> 251 <213> ORGANISM: Artificial
253 <220> FEATURE:
254 <223> OTHER INFORMATION: amplification primer
256 <400> SEQUENCE: 11
E--> 257 cgtactgccttatagggttc t do not show "t" in the sequence itself. Use "n" and
260 <210> SEQ ID NO: 22
261 <211> LENGTH: 23
262 <212> TYPE: DNA
C--> 263 <213> ORGANISM: Artificial
265 <220> FEATURE:
266 <223> OTHER INFORMATION: amplification primer
268 <400> SEQUENCE: 22
E--> 269 gmatgtgmta mggtmtmdmid gdc invalid - use n and explain
272 <210> SEQ ID NO: 23
273 <211> LENGTH: 20
274 <212> TYPE: DNA
C--> 275 <213> ORGANISM: Artificial
277 <220> FEATURE:
278 <223> OTHER INFORMATION: amplification primer
280 <400> SEQUENCE: 23
E--> 281 cgtactgccttatagggttc invalid
284 <210> SEQ ID NO: 24
285 <211> LENGTH: 21
286 <212> TYPE: DNA
C--> 287 <213> ORGANISM: Artificial
289 <220> FEATURE:
290 <223> OTHER INFORMATION: amplification primer
292 <400> SEQUENCE: 24
E--> 293 cgtamtgmttatagggttc invalid
296 <210> SEQ ID NO: 25

see item 11
on seq summary sheet

Use "n" and
explain in
<220>-<223>
section
(for sequence
header)

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/530,746

DATE: 04/30/2001
TIME: 17:59:38

Input Set : A:\4817 0Q.txt

Output Set: N:\CRF3\04302001\I530746.raw

297 <211> LENGTH: 23
298 <212> TYPE: DNA
C--> 299 <213> ORGANISM: Artificial *rem 11*
301 <220> FEATURE:
302 <223> OTHER INFORMATION: amplification primer
304 <400> SEQUENCE: 25
E--> 305 gmatgppp mgtmtmdmid gdm *invalid - use "n" and explain* 23
308 <210> SEQ ID NO: 16
309 <211> LENGTH: 26
310 <212> TYPE: DNA
C--> 311 <213> ORGANISM: Artificial *rem 11*
313 <220> FEATURE:
314 <223> OTHER INFORMATION: amplification primer
316 <400> SEQUENCE: 26
E--> 317 cgtamtgmmt tatagggttm *invalid* 20
332 <210> SEQ ID NO: 28
333 <211> LENGTH: 21
334 <212> TYPE: DNA
C--> 335 <213> ORGANISM: Artificial
337 <220> FEATURE:
338 <223> OTHER INFORMATION: amplification primer
340 <400> SEQUENCE: 28
E--> 341 cgtamtgmmt tatagggttc *invalid* 21
344 <210> SEQ ID NO: 29
345 <211> LENGTH: 26
346 <212> TYPE: DNA
C--> 347 <213> ORGANISM: Artificial
349 <220> FEATURE:
350 <223> OTHER INFORMATION: amplification primer
352 <400> SEQUENCE: 29
E--> 353 gmatgtgmta mgtmtmdmid gdmmttc *invalid* 26
356 <210> SEQ ID NO: 30
357 <211> LENGTH: 20
358 <212> TYPE: DNA
C--> 359 <213> ORGANISM: Artificial
361 <220> FEATURE:
362 <223> OTHER INFORMATION: amplification primer
364 <400> SEQUENCE: 30
E--> 365 cgtamtgmmt tatagggttc *invalid* 20
368 <210> SEQ ID NO: 31
369 <211> LENGTH: 26
370 <212> TYPE: DNA
C--> 371 <213> ORGANISM: Artificial
373 <220> FEATURE:
374 <223> OTHER INFORMATION: amplification primer
376 <400> SEQUENCE: 31
E--> 377 gmatgtgmta mgtmtmdmid gdmmttc *invalid* 26
380 <210> SEQ ID NO: 32
381 <211> LENGTH: 26

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/530,746

DATE: 04/30/2001
 TIME: 17:54:38

Input Set : A:\4817 00.txt
 Output Set: N:\CRF3\04302001\I530746.raw

```

382 <210> TYPE: DNA
C--> 383 <213> ORGANISM: Artificial
385 <214> FEATURE
386 <215> OTHER INFORMATION: amplification primer
388 <400> SEQUENCE 32
E--> 389 gmatgpkppa mggtmtmdmid gdmptm 26
416 <210> SEQ ID NO: 35
417 <211> LENGTH: 18
418 <212> TYPE: DNA
C--> 419 <213> ORGANISM: Artificial
421 <214> FEATURE
422 <215> OTHER INFORMATION: amplification primer
424 <400> SEQUENCE 35
E--> 425 cgtamtgmmt tatagggt 18
428 <210> SEQ ID NO: 36
429 <211> LENGTH: 17
430 <212> TYPE: DNA
C--> 431 <213> ORGANISM: Artificial
433 <214> FEATURE
434 <215> OTHER INFORMATION: amplification primer
436 <400> SEQUENCE 16
E--> 437 gmatgtgmta mggtmtamia gamttmc 27
440 <210> SEQ ID NO: 37
441 <211> LENGTH: 17
442 <212> TYPE: DNA
C--> 443 <213> ORGANISM: Artificial
445 <214> FEATURE
446 <215> OTHER INFORMATION: amplification primer
448 <400> SEQUENCE 37
E--> 449 gmatgtgmta mggtmtamia gamptmc 27
452 <210> SEQ ID NO: 38
453 <211> LENGTH: 17
454 <212> TYPE: DNA
C--> 455 <213> ORGANISM: Artificial
457 <214> FEATURE
458 <215> OTHER INFORMATION: amplification primer
460 <400> SEQUENCE 38
E--> 461 gmatgtgmta mggtmtamia gamptmm 27
464 <210> SEQ ID NO: 39
465 <211> LENGTH: 18
466 <212> TYPE: DNA
C--> 467 <213> ORGANISM: Artificial
469 <214> FEATURE
470 <215> OTHER INFORMATION: amplification primer
472 <400> SEQUENCE 39
E--> 473 cgtdmtgmmt idtdgggt 18
476 <210> SEQ ID NO: 40
477 <211> LENGTH: 17
478 <212> TYPE: DNA

```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/530,746

DATE: 04/30/2001
TIME: 17:59:38

Input Set : A:\4817 00.txt
Output Set: N:\CRF3\04302001\I530746.raw

```

C--> 479 <213> ORGANISM: Artificial
      481 <220> FEATURE:
      482 <223> OTHER INFORMATION: amplification primer
      484 <400> SEQUENCE: 40
E--> 485 gmatgppppa mggtmtamia gampmtmc 27
      488 <210> SEQ ID NO: 41
      489 <211> LENGTH: 27
      490 <212> TYPE: DNA
C--> 491 <213> ORGANISM: Artificial
      493 <220> FEATURE:
      494 <223> OTHER INFORMATION: amplification primer
      496 <400> SEQUENCE: 41
E--> 497 gmatgppppa mggtmtamia gampmtm 27
      512 <210> SEQ ID NO: 43
      513 <211> LENGTH: 27
      514 <212> TYPE: DNA
C--> 515 <213> ORGANISM: Artificial
      517 <220> FEATURE:
      518 <223> OTHER INFORMATION: amplification primer
      520 <400> SEQUENCE: 43
E--> 521 gmatgtgmta mggtmtimga gaamtmc 27
      524 <210> SEQ ID NO: 44
      525 <211> LENGTH: 27
      526 <212> TYPE: DNA
C--> 527 <213> ORGANISM: Artificial
      528 <220> FEATURE:
      529 <223> OTHER INFORMATION: amplification primer
      531 <400> SEQUENCE: 44
E--> 532 gmatgtgmta mggtmtimga gaktmtc 27
      1109 <210> SEQ ID NO: 93
      1110 <211> LENGTH: 61
      1111 <212> TYPE: DNA
      1112 <213> ORGANISM: HCV
      1114 <400> SEQUENCE: 93
E--> 1115 ggtactgcct gataggggtgc ttgcgagtgcc ccggggaggt ctcgtagacc
E--> 1116 gtgcaccatg a
      1119 <210> SEQ ID NO: 94
      1120 <211> LENGTH: 61
      1121 <212> TYPE: DNA
      1122 <213> ORGANISM: HGBV-B
      1124 <400> SEQUENCE: 94
E--> 1125 cgtactgcct gataggggtcc ttgcgagggg atctgggaggt ctcgtagacc
E--> 1126 gttagcacatg c

```

These two error types exist
throughout Sequence Listing

50 ← insert cumulative
61 base total at
right margin of
each line

(61) 50
61 ←

The types of errors shown exist throughout the Sequence Listing. Please check
all sequences for similar errors.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/530,746

DATE: 04/30/2001
TIME: 17:59:39

Input Set : A:\4817 00.txt
Output Set: N:\CRF3\04302001\I530746.raw

L:13 M:277 C: Current Application Number differs. Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs. Replaced Current Filing Date
L:23 M:221 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 1
L:35 M:221 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 2
L:47 M:222 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 3
L:59 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 4
L:71 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 5
L:119 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 10
L:131 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 11
L:143 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 12
L:155 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 13
L:167 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 14
L:179 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 15
L:191 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 16
L:203 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 17
L:215 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 18
L:227 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 19
L:239 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 20
L:251 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 21
L:257 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:267 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 22
L:269 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:275 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 23
L:281 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:287 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 24
L:293 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:299 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 25
L:305 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:311 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 26
L:317 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:323 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 27
L:335 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 28
L:341 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:347 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 29
L:353 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:359 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 30
L:365 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:371 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 31
L:377 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:383 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 32
L:389 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:395 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 33
L:407 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 34
L:419 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 35
L:425 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:431 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 36
L:437 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:443 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 37

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/530,746

DATE: 04/30/2001

TIME: 17:59:39

Input Set : A:\4817 00.txt

Output Set: N:\CRF3\04302001\I530746.raw

L:449 M:321 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:455 M:321 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 38
 L:461 M:321 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:467 M:321 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 39
 L:473 M:321 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:479 M:321 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 40
 L:485 M:321 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
 L:491 M:321 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 41
 L:497 M:321 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
 L:503 M:321 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 42
 L:515 M:321 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 43
 L:521 M:321 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:527 M:321 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 44
 L:533 M:321 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:539 M:321 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 45
 L:545 M:321 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
 L:551 M:321 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 46
 L:557 M:321 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 47
 L:563 M:321 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:569 M:321 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 48
 L:575 M:321 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:581 M:321 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 49
 L:587 M:321 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
 L:593 M:321 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 50
 L:599 M:321 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 51
 L:605 M:321 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 52
 L:611 M:321 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 53
 L:617 M:321 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 54
 L:1115 M:254 E: No. of Bases conflict, LENGTH:Input:61 Counted:50 SEQ:93
 M:254 Repeated in SeqNo=93
 L:1125 M:254 E: No. of Bases conflict, LENGTH:Input:61 Counted:50 SEQ:94
 M:254 Repeated in SeqNo=94